

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/934,254DATE: 03/26/98
TIME: 18:19:17

INPUT SET: S24406.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Thomas, Terry L.

(ii) TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
DELTA 6-DESATURASE

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Scully, Scott, Murphy & Presser

(B) STREET: 400 Garden City Plaza

(C) CITY: Garden City

(D) STATE: New York

(E) COUNTRY: United States

(F) ZIP: 11530

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Presser, Leopold

(B) REGISTRATION NUMBER: 19,827

(C) REFERENCE/DOCKET NUMBER: 8383ZYXWVU

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (516) 742-4343

(B) TELEFAX: (516) 742-4366

(C) TELEX: 230 901 SANS UR

(2) INFORMATION FOR SEQ ID NO:1:

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47
48 (i) SEQUENCE CHARACTERISTICS:
49
50 (A) LENGTH: 3588 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: both
53 (D) TOPOLOGY: linear
54
55 (ii) MOLECULE TYPE: DNA (genomic)
56
57 (ix) FEATURE:
58
59 (A) NAME/KEY: CDS
60 (B) LOCATION: 2002..3081
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCC GTATTCTGAA 60
65
66 TCCCCGCATT CGCATTGTTA ATCGTTTGTT CAACCATGCC CTGGGTAAAC GTTTAGACAC 120
67
68 CACCTTGCCA GACCACGTTA GTTTGAGTGT TTCCGCCCTG GCGGCCCCGA TTTTTCCTT 180
69
70 TGC GGCTTTG GGCAATCAGG CGATCGGGCA ATTGCGTTTG TTTGACCAGA CTTGGCCCAT 240
71
72 TCAGGAAATT GTCATTCACC AAGACCATCC CTGGCTCAAT TTACCCCTGG CGGATTTATG 300
73
74 GGATGATCCG AGCCGAATGT TGATCTATTA CCTACCGGCC CACAGTGAAA CGGATTTAGT 360
75
76 AGGCGCAGTG GTGAATAATT TAACGTTGCA ATCTGGGGAC CATTTAATAG TGGGACAAAA 420
77
78 ACCCCAACCC AAGACCAAAC GGCGATCGCC TTGGCGCAA TTTTCCAAAC TGATTACCAA 480
79
80 CCTGCGGGAG TATCAGCGGT ATGTCCAACA GGTGATATGG GTGGTGTTGT TTTTATTGTT 540
81
82 GATGATTTTT CTGGCCACCT TCATCTACGT TTCCATTGAT CAACATATTG CCCCAGTGGA 600
83
84 CGCGTTGTAT TTTTCCGTGG GCATGATTAC CGGGGCCGGT GGCAAGGAAG AGGTGGCCGA 660
85
86 AAAGTCCCCC GATATCATCA AAGTATTCAC AGTGGTGATG ATGATCGCCG GGGCGGGGGT 720
87
88 GATTGGTATT TGTTATGCCC TACTGAATGA TTTCATCCTT GGCAGTCGCT TTAGTCAGTT 780
89
90 TTTGGATGCG GCCAAGTTAC CCGATCGCCA TCACATCATC ATTTGTGGGC TGGGGGGAGT 840
91
92 GAGCATGGCC ATTATTGAAG AGTTAATTCA CCAGGGCCAT GAAATTGTGG TAATCGAAAA 900
93
94 GGATACAGAT AATCGTTTCT TGCATACGGC CCGCTCCCTG GGGGTGCCCC TAATTGTGGA 960
95
96 GGATGCCCCG CTAGAAAGAA CGTTGGCCTG CGCCAATATC AACCGAGCCG AAGCCATTGT 1020
97
98 GGTGGCCACC AGCGACGACA CCGTTAACTT GGAAATTGGC CTAAGTCCCA AGGCGATCGC 1080
99

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100	CCCTAGCCTG CCAGTGGTGT TGC GTTGCCA GGATGCCCAG TTTAGCCTGT CCCTGCAGGA	1140
101		
102	AGTATTTGAA TTTGAAACGG TGCTTTGTCC GGC GGAATTG GCCACCTATT CCTTTGCGGC	1200
103		
104	GGCGGCCCTG GGGGGCAAAA TTTTGGGCAA CGGCATGACC GATGATTTGC TGTGGGTAGC	1260
105		
106	CCTAGCCACC TTAATCACTC CTAACCATCC CTTTGCCGAC CAATTGGTTA AAATTGCAGC	1320
107		
108	CCAAAAGTCT GATTTTCGTTT CCCTCTATCT AGAACGGGGT GGCAAAACCA TCCATAGCTG	1380
109		
110	GGAATTATTG GGTACCCATC TCGACTCTGG AGACGTGTTG TATTTAACCA TGCCCGCCAC	1440
111		
112	TGCCCTAGAG CAACTTTGGC GATCGCCCCG TGCCACTGCT GATCCTCTGG ACTCTTTTTT	1500
113		
114	GGTTTAGCAT GGGGGGATGG AACTCTTGAC TCGGCCCAAT GGTGATCAAG AAAGAACGCT	1560
115		
116	TTGTCTATGT TTAGTATTTT TAAGTTAACC AACAGCAGAG GATAACTTCC AAAAGAAATT	1620
117		
118	AAGCTCAAAA AGTAGCAAAA TAAGTTTAAT TCATAACTGA GTTTTACTGC TAAACAGCGG	1680
119		
120	TGCAAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATATTGTGA CCATGGTTCC	1740
121		
122	CAGGCATCTG CTCTAGGGAG TTTTCCCGCT GCCTTTAGAG AGTATTTTCT CCAAGTCGGC	1800
123		
124	TAAC TCCCCC ATTTT TAGGC AAAATCATAT ACAGACTATC CCAATATTGC CAGAGCTTTG	1860
125		
126	ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG ACTCCCAGTT GGAATAAATT	1920
127		
128	TTTAGTCTCC CCCGGCGCTG GAGTTTTTTT GTAGTTAATG GCGGTATAAT GTGAAAGTTT	1980
129		
130	TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA AGA ATT AAA TTT ACC	2031
131		
132		
133		
134	CAG AAA CGG GGG TTT CGT CGG GTA CTA AAC CAA CGG GTG GAT GCC TAC	2079
135	Gln Lys Arg Gly Phe Arg Arg Val Leu Asn Gln Arg Val Asp Ala Tyr	
136		
137		
138	TTT GCC GAG CAT GGC CTG ACC CAA AGG GAT AAT CCC TCC ATG TAT CTG	2127
139	Phe Ala Glu His Gly Leu Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu	
140		
141		
142	AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG GCC TTT GTG	2175
143	Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp Ala Phe Val	
144		
145		
146	CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC CTA CTG GGT TGT ATG GTT	2223
147	Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Leu Gly Cys Met Val	
148		
149		
150	TTG GCG ATC GCC TTG GCG GCC TTT TCC TTC AAT GTC GGC CAC GAT GCC	2271
151	Leu Ala Ile Ala Leu Ala Ala Phe Ser Phe Asn Val Gly His Asp Ala	
152		

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153																		
154	AAC	CAC	AAT	GCC	TAT	TCC	TCC	AAT	CCC	CAC	ATC	AAC	CGG	GTT	CTG	GGC		2319
155	Asn	His	Asn	Ala	Tyr	Ser	Ser	Asn	Pro	His	Ile	Asn	Arg	Val	Leu	Gly		
156					95					100					105			
157																		
158	ATG	ACC	TAC	GAT	TTT	GTC	GGG	TTA	TCT	AGT	TTT	CTT	TGG	CGC	TAT	CGC		2367
159	Met	Thr	Tyr	Asp	Phe	Val	Gly	Leu	Ser	Phe	Leu	Trp	Arg	Tyr	Arg			
160				110					115				120					
161																		
162	CAC	AAC	TAT	TTG	CAC	CAC	ACC	TAC	ACC	AAT	ATT	CTT	GGC	CAT	GAC	GTG		2415
163	His	Asn	Tyr	Leu	His	His	Thr	Tyr	Thr	Asn	Ile	Leu	Gly	His	Asp	Val		
164			125					130					135					
165																		
166	GAA	ATC	CAT	GGA	GAT	GGC	GCA	GTA	CGT	ATG	AGT	CCT	GAA	CAA	GAA	CAT		2463
167	Glu	Ile	His	Gly	Asp	Gly	Ala	Val	Arg	Met	Ser	Pro	Glu	Gln	Glu	His		
168		140					145					150						
169																		
170	GTT	GGT	ATT	TAT	CGT	TTC	CAG	CAA	TTT	TAT	ATT	TGG	GGT	TTA	TAT	CTT		2511
171	Val	Gly	Ile	Tyr	Arg	Phe	Gln	Gln	Phe	Tyr	Ile	Trp	Gly	Leu	Tyr	Leu		
172		155				160					165					170		
173																		
174	TTC	ATT	CCC	TTT	TAT	TGG	TTT	CTC	TAC	GAT	GTC	TAC	CTA	GTG	CTT	AAT		2559
175	Phe	Ile	Pro	Phe	Tyr	Trp	Phe	Leu	Tyr	Asp	Val	Tyr	Leu	Val	Leu	Asn		
176					175					180					185			
177																		
178	AAA	GGC	AAA	TAT	CAC	GAC	CAT	AAA	ATT	CCT	CCT	TTC	CAG	CCC	CTA	GAA		2607
179	Lys	Gly	Lys	Tyr	His	Asp	His	Lys	Ile	Pro	Pro	Phe	Gln	Pro	Leu	Glu		
180				190					195					200				
181																		
182	TTA	GCT	AGT	TTG	CTA	GGG	ATT	AAG	CTA	TTA	TGG	CTC	GGC	TAC	GTT	TTC		2655
183	Leu	Ala	Ser	Leu	Leu	Gly	Ile	Lys	Leu	Leu	Trp	Leu	Gly	Tyr	Val	Phe		
184			205					210					215					
185																		
186	GGC	TTA	CCT	CTG	GCT	CTG	GGC	TTT	TCC	ATT	CCT	GAA	GTA	TTA	ATT	GGT		2703
187	Gly	Leu	Pro	Leu	Ala	Leu	Gly	Phe	Ser	Ile	Pro	Glu	Val	Leu	Ile	Gly		
188		220					225					230						
189																		
190	GCT	TCG	GTA	ACC	TAT	ATG	ACC	TAT	GGC	ATC	GTG	GTT	TGC	ACC	ATC	TTT		

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206  GGT TTA AAT CAC CAA GTT ACC CAC CAT CTT TTC CCC AAT ATT TGT CAT      2943
207  Gly Leu Asn His Gln Val Thr His His Leu Phe Pro Asn Ile Cys His
208      300                      305                      310
209
210  ATT CAC TAT CCC CAA TTG GAA AAT ATT ATT AAG GAT GTT TGC CAA GAG      2991
211  Ile His Tyr Pro Gln Leu Glu Asn Ile Ile Lys Asp Val Cys Gln Glu
212  315                      320                      325                      330
213
214  TTT GGT GTG GAA TAT AAA GTT TAT CCC ACC TTC AAA GCG GCG ATC GCC      3039
215  Phe Gly Val Glu Tyr Lys Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala
216      335                      340                      345
217
218  TCT AAC TAT CGC TGG CTA GAG GCC ATG GGC AAA GCA TCG TGACATTGCC      3088
219  Ser Asn Tyr Arg Trp Leu Glu Ala Met Gly Lys Ala Ser
220      350                      355
221
222  TTGGGATTGA AGCAAAATGG CAAAATCCCT CGTAAATCTA TGATCGAAGC CTTTCTGTGTG      3148
223
224  CCCGCCGACC AAATCCCCGA TGCTGACCAA AGGTTGATGT TGGCATTGCT CCAAACCCAC      3208
225
226  TTTGAGGGGG TTCATTGGCC GCAGTTTCAA GCTGACCTAG GAGGCAAAGA TTGGGTGATT      3268
227
228  TTGCTCAAAT CCGCTGGGAT ATTGAAAGGC TTCACCACCT TTGGTTTCTA CCCTGCTCAA      3328
229
230  TGGGAAGGAC AAACCGTCAG AATTGTTTAT TCTGGTGACA CCATCACCGA CCCATCCATG      3388
231
232  TGGTCTAACC CAGCCCTGGC CAAGGCTTGG ACCAAGGCCA TGCAAATTCT CCACGAGGCT      3448
233
234  AGGCCAGAAA AATTATATTG GCTCCTGATT TCTTCCGGCT ATCGCACCTA CCGATTTTTG      3508
235
236  AGCATTTTTG CCAAGGAATT CTATCCCCAC TATCTCCATC CCACTCCCCC GCCTGTACAA      3568
237
238  AATTTTATCC ATCAGCTAGC      3588
239
240
241  (2) INFORMATION FOR SEQ ID NO:2:
242
243      (i) SEQUENCE CHARACTERISTICS:
244
245          (A) LENGTH: 359 amino acids
246          (B) TYPE: amino acid
247          (D) TOPOLOGY: linear
248
249      (ii) MOLECULE TYPE: protein
250
251      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
252
253  Met Leu Thr Ala Glu Arg Ile Lys Phe Thr Gln Lys Arg Gly Phe Arg
254      1                      5                      10                      15
255
256  Arg Val Leu Asn Gln Arg Val Asp Ala Tyr Phe Ala Glu His Gly Leu
257      20                      25                      30
258

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***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

878 (2) INFORMATION FOR SEQ ID NO:25:

879

880 (i) SEQUENCE CHARACTERISTICS:

881

882 (A) LENGTH: 5 amino acids

883 (B) TYPE: amino acid

884 (D) TOPOLOGY: linear

885

886 (ii) MOLECULE TYPE: Peptide

887

888 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

889

890 His Val Pro His His

891

1 5

892

893

1045 (2) INFORMATION FOR SEQ ID NO:27:

1046

1047 (i) SEQUENCE CHARACTERISTICS:

1048 (A) LENGTH: 452 amino acids

1049 (B) TYPE: amino acid

1050 (D) TOPOLOGY: linear

1051

1052 (ii) MOLECULE TYPE: protein

1053

1054 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

1055

1056 Met Glu Gly Glu Ala Lys Lys Tyr Ile Thr Ala Glu Asp Leu Arg Arg

1057

1

5

10

15

1058

1059 His Asn Lys Ser Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Val Tyr

1060

20

25

30

1061

1062 Asp Cys Ser Arg Trp Ala Ala Glu His Pro Gly Gly Glu Val Pro Leu

1063

35

40

45

1064

1065 Leu Ser Leu Ala Gly Gln Asp Val Thr Asp Ala Phe Ile Ala Tyr His

1066

50

55

60

1067

1068 Pro Gly Thr Ala Trp Arg His Leu Asp Pro Leu Phe Thr Gly Tyr Tyr

1069

65

70

75

80

1070

1071 Tyr Leu Lys Asp Phe Glu Val Ser Glu Ile Ser Lys Asp Tyr Arg Arg

1072

85

90

95

1073

1074 Leu Leu Asn Glu Met Ser Arg Ser Gly Ile Phe Glu Lys Lys Gly His

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	100	105	110
1075			
1076			
1077	His Ile Met Trp Thr Phe Val Gly Val Ala Val Met Met Ala Ala Ile		
1078	115	120	125
1079			
1080	Val Tyr Gly Val Leu Ala Ser Glu Ser Val Gly Val His Met Leu Cys		
1081	130	135	140
1082			
1083	Gly Ala Leu Leu Gly Leu Leu Trp Ile Gln Ala Ala Tyr Val Gly His		
1084	145	150	155
1085			
1086	Asp Ser Gly His Tyr Gln Val Met Pro Thr Arg Gly Tyr Asn Arg Ile		
1087	165	170	175
1088			
1089	Thr Gln Leu Ile Ala Gly Asn Ile Leu Thr Gly Ile Ser Ile Ala Trp		
1090	180	185	190
1091			
1092	Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp		
1093	195	200	205
1094			
1095	Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser Thr Arg		
1096	210	215	220
1097			
1098	Leu Phe Asn Ser Ile Thr Ser Val Phe Tyr Gly Arg Val Leu Lys Phe		
1099	225	230	235
1100			
1101	Asp Glu Val Ala Arg Phe Leu Val Ser Tyr Gln His Trp Thr Tyr Tyr		
1102	245	250	255
1103			
1104	Pro Val Met Ile Phe Gly Arg Val Asn Leu Phe Ile Gln Thr Phe Leu		
1105	260	265	270
1106			
1107	Leu Leu Leu Thr Arg Arg Asp Val Pro Asp Arg Ala Leu Asn Leu Met		
1108	275	280	285
1109			
1110	Gly Ile Ala Val Phe Trp Thr Trp Phe Pro Leu Phe Val Ser Cys Leu		
1111	290	295	300
1112			
1113	Pro Asn Trp Pro Glu Arg Phe Gly Phe Val Leu Ile Ser Phe Ala Val		
1114	305	310	315
1115			
1116	Thr Ala Ile Gln His Val Gln Phe Thr Leu Asn His Phe Ser Gly Asp		
1117	325	330	335
1118			
1119	Thr Tyr Val Gly Pro Pro Lys Gly Asp Asn Trp Phe Glu Lys Gln Thr		
1120	340	345	350
1121			
1122	Lys Gly Thr Ile Asp Ile Thr Cys Pro Pro Trp Met Asp Trp Phe Phe		
1123	355	360	365
1124			
1125	Gly Gly Leu Gln Phe Gln Leu Glu His His Leu Phe Pro Arg Leu Pro		
1126	370	375	380
1127			

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1128	Arg Gly Gln Leu Arg Lys Ile Ala Pro Leu Ala Arg Asp Leu Cys Lys	
1129	385	390 395 400
1130		
1131	Lys His Gly Met Pro Tyr Arg Ser Phe Gly Phe Trp Asp Asp Ala Asn	
1132		405 410 415
1133		
1134	Val Arg Thr Ile Arg Thr Leu Arg Asp Ala Ala Val Gln Ala Arg Asp	
1135		420 425 430
1136		
1137	Leu Asn Ser Ala Pro Cys Pro Lys Lys Leu Gly Tyr Gly Glu Ala Tyr	
1138		435 440 445
1139		
1140	Asn Thr His Gly	
1141		450
1142		

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SEQUENCE VERIFICATION REPORT
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Original Text